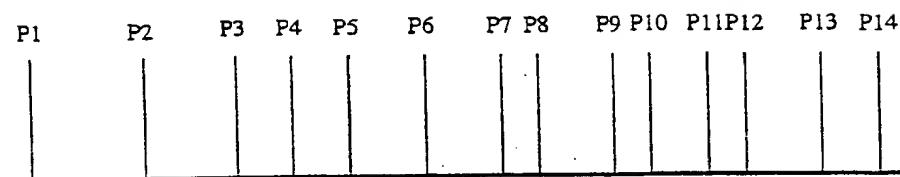
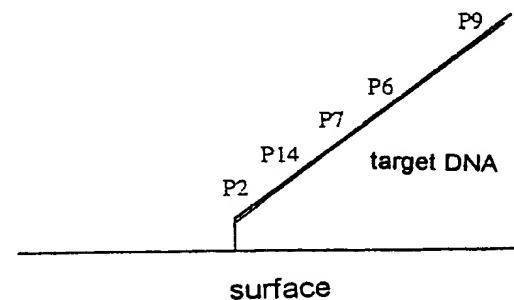


1. Mass distribution of the probes



2. Hybridization



3. Mass distribution of the hybridized probes

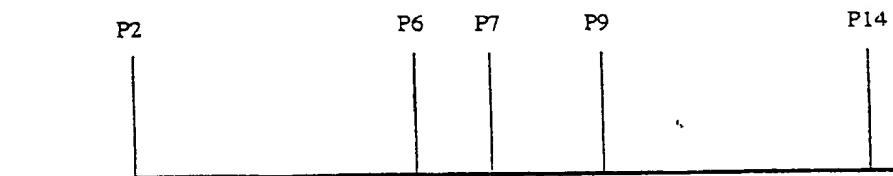
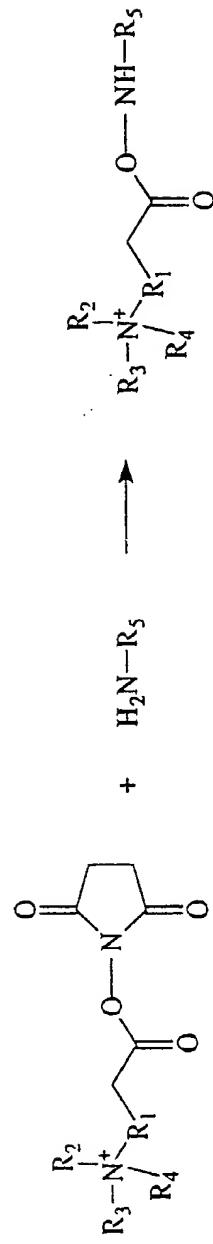


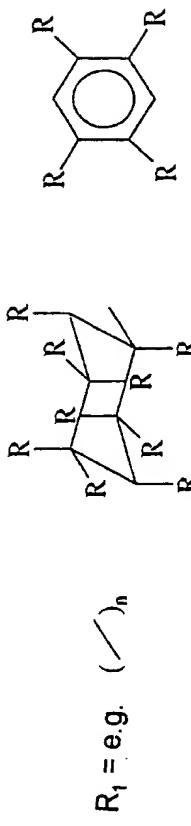
Fig. 1

N-terminal mass/charge tagging

Fig. 2

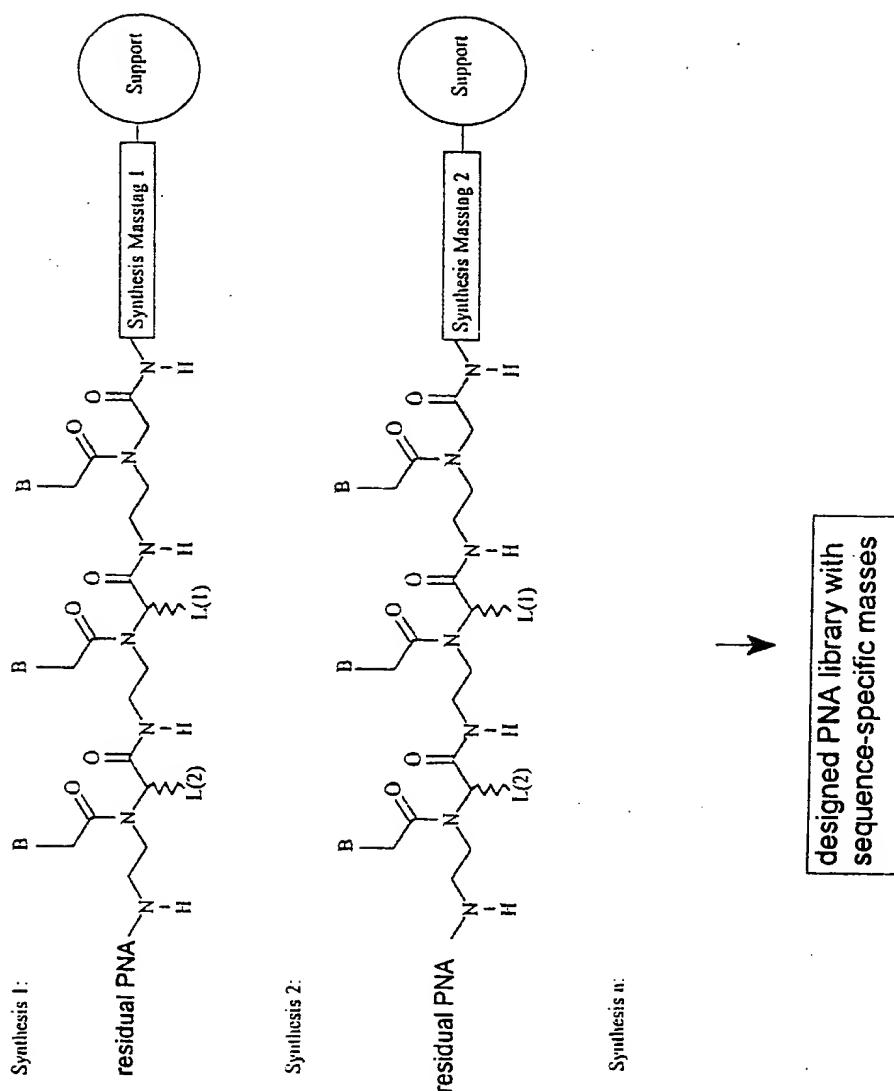


$R =$ e.g. alkyl, $-CH_3$, $-C_2H_5$, $-C_3H_7$, $-C_4H_9$ etc.



$R_{2,4} =$ e.g. alkyl, substituted alkyl

$R_5 =$ e.g. nucleic acid, PNA, methyl phosphonate nucleic acid, phosphorothioate nucleic acid



B = adenine, cytosine, guanine, thymine or purine or pyrimidine derivatives or their deaza analogues

$L(n)$ are various sets of substituents, selected specifically for each base, which are inserted in each synthesis step in order to obtain minimized peak overlaps in the MALDI-MS.

Fig. 3

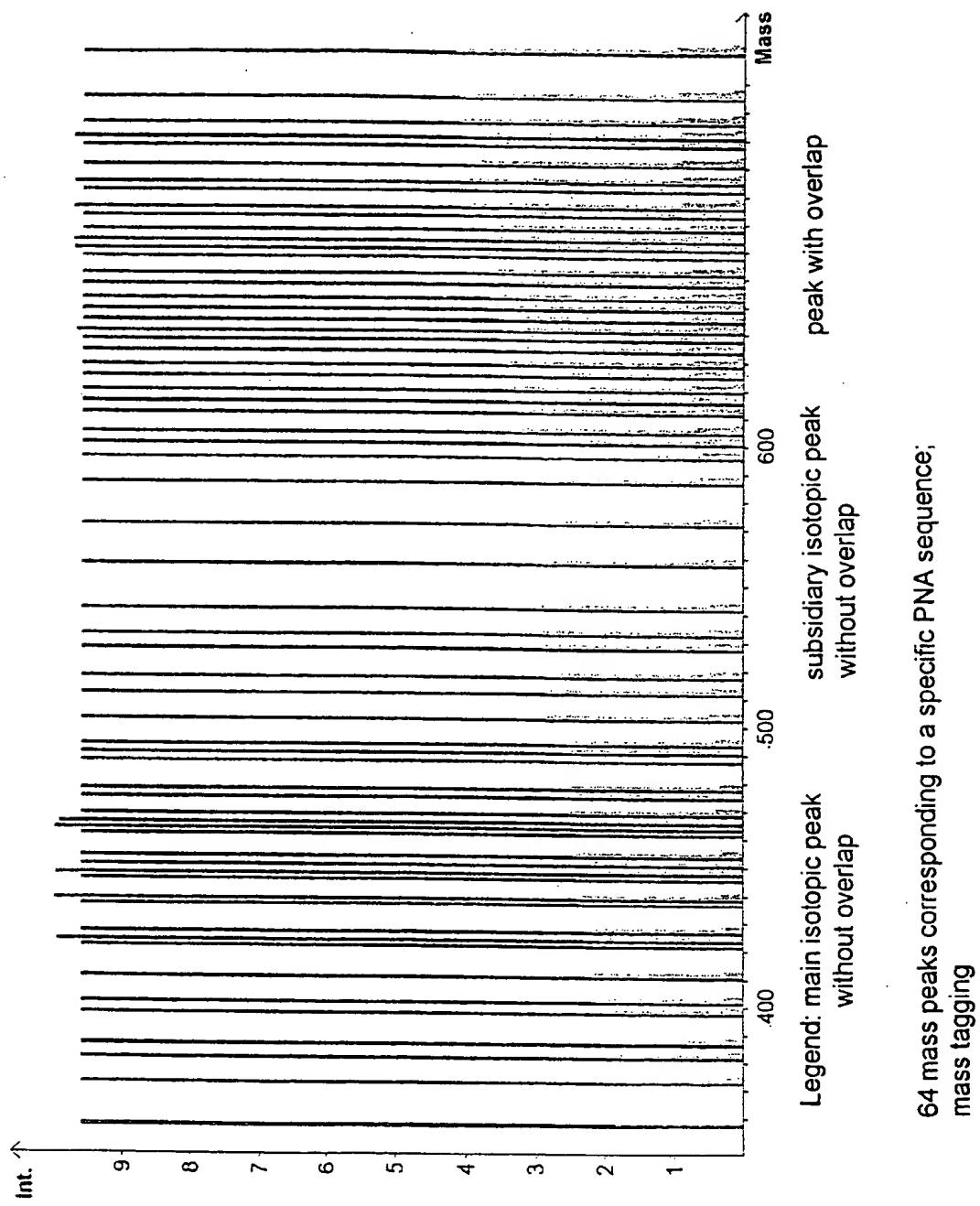


Fig. 4

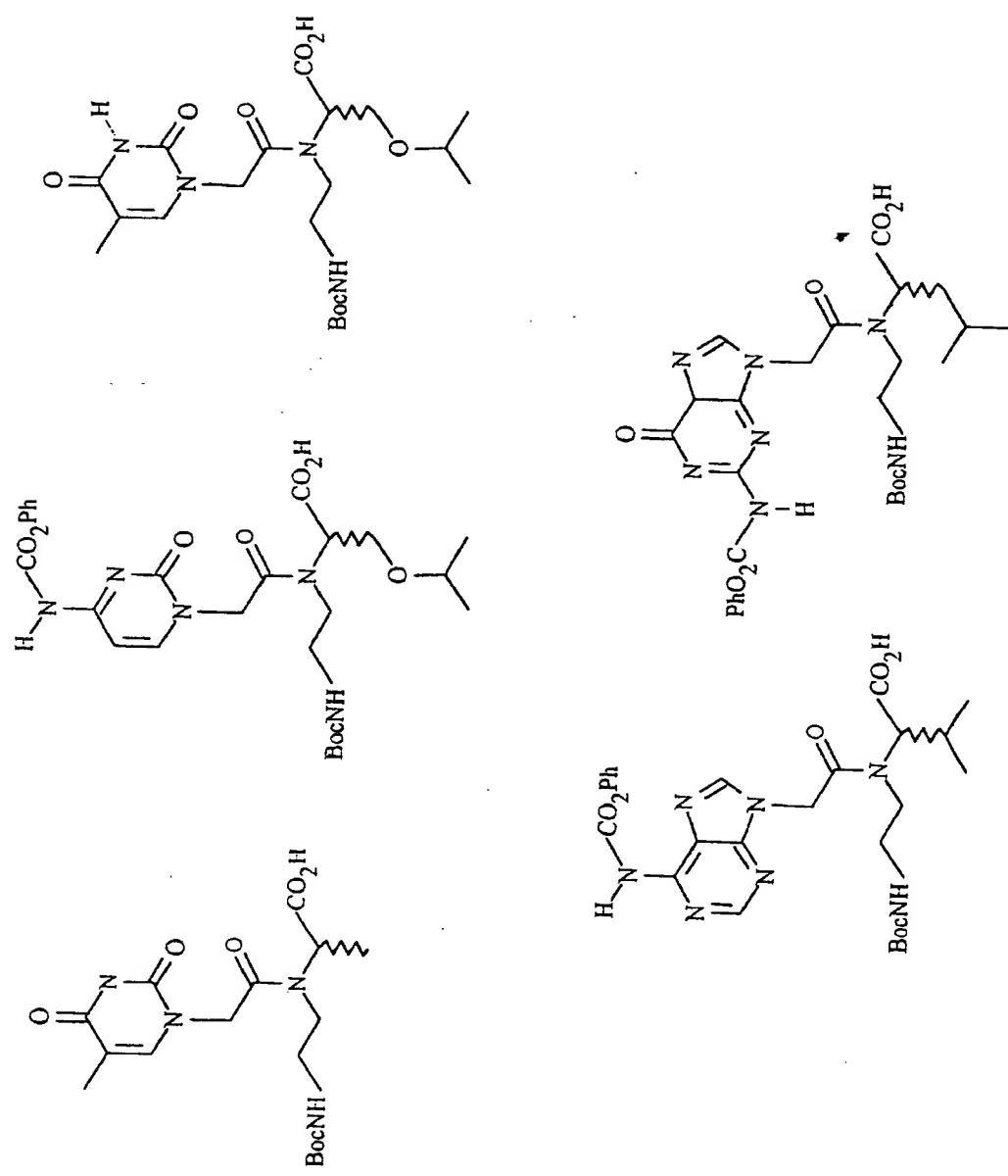


Fig. 5

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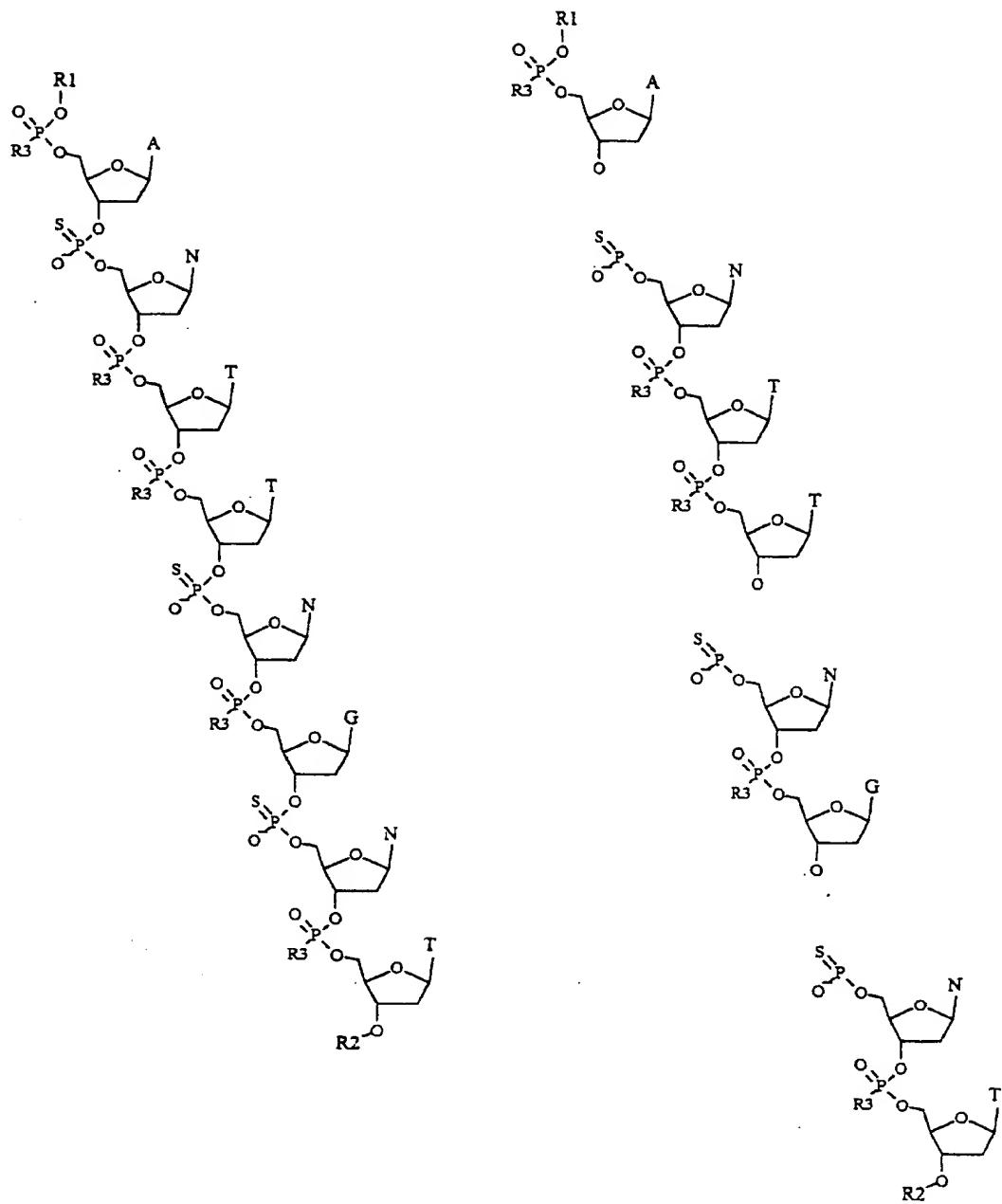


Fig. 6